SEQUENCE LISTING

<110> Kodama, Tatsuhiko Yamada, Yoshiki Kamada, Nobuo Jishage, Kou-ichi

<120> Nonhuman animals for antibody production, and methods and systems for producing antibodies using such animals

<130> 14875-167US1 <150> PCT/JP2005/006298 <151> 2005-03-31 <150> JP2004-107669 <151> 2004-03-31 <160> 10 <170> PatentIn version 3.1 <210> 1 <211> 1539 <212> DNA <213> Baculovirus <220> <221> CDS <222> (1)..(1539) <400> 1 atg gta agc gct att gtt tta tat gtg ctt ttg gcg gcg gcg gcg cat 48 Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala His tct gcc ttt gcg gcg gag cac tgc aac gcg caa atg aag acg ggt ccg 96 Ser Ala Phe Ala Ala Glu His Cys Asn Ala Gln Met Lys Thr Gly Pro 25 20 tac aag att aaa aac ttg gac att acc ccg ccc aag gaa acg ctg caa 144 Tyr Lys Ile Lys Asn Leu Asp Ile Thr Pro Pro Lys Glu Thr Leu Gln 35 aag gac gtg gaa atc acc atc gtg gag acg gac tac aac gaa aac gtg 192 Lys Asp Val Glu Ile Thr Ile Val Glu Thr Asp Tyr Asn Glu Asn Val 50 55 att atc ggc tac aag ggg tac tac cag gcg tat gcg tac aac ggc ggc 240 Ile Ile Gly Tyr Lys Gly Tyr Tyr Gln Ala Tyr Ala Tyr Asn Gly Gly 65 70 tcg ctg gat ccc aac aca cgc gtc gaa gaa acc atg aaa acg ctg aat 288 Ser Leu Asp Pro Asn Thr Arg Val Glu Glu Thr Met Lys Thr Leu Asn 90

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-		_		ctc Leu 230			_	-						720
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				aag Lys										864
				gga Gly										912
				atg Met 310										960

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		acc Thr															1392
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gtg Val	att Ile	tta Leu	ttt Phe 500	ttg Leu	tac Tyr	tgt Cys	atg Met	att Ile 505	aga Arg	aac Asn	cgt Arg	aat Asn	aga Arg 510	Gln	tat Tyr		1536
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Val Thr Arg Glu His Cys Leu Ile Asp Asn Asp Ile Tyr Asp Leu Ser

Lys Ala Ala Cys Leu Leu Ile Lys Asp Asp Lys Asn Asn Pro Glu Ser

235

230

245

Lys Asn Thr Trp Asn Cys Lys Phe Asn Arg Cys Ile Lys Arg Lys Val

Glu His Arg Val Lys Lys Arg Pro Pro Thr Trp Arg His Asn Val Arg 275 280 285

Ala Lys Tyr Thr Glu Gly Asp Thr Ala Thr Lys Gly Asp Leu Met His 290 295 300

Ile Gln Glu Glu Leu Met Tyr Glu Asn Asp Leu Leu Lys Met Asn Ile 305 Glu Leu Met His Ala His Ile Asn Lys Leu Asn Asn Met Leu His Asp 330 325 Leu Ile Val Ser Val Ala Lys Val Asp Glu Arg Leu Ile Gly Asn Leu Met Asn Asn Ser Val Ser Ser Thr Phe Leu Ser Asp Asp Thr Phe Leu 360 Leu Met Pro Cys Thr Asn Pro Pro Ala His Thr Ser Asn Cys Tyr Asn 380 370 375 Asn Ser Ile Tyr Lys Glu Gly Arg Trp Val Ala Asn Thr Asp Ser Ser 390 395 Gln Cys Ile Asp Phe Ser Asn Tyr Lys Glu Leu Ala Ile Asp Asp Asp 405 410 Val Glu Phe Trp Ile Pro Thr Ile Gly Asn Thr Thr Tyr His Asp Ser 420 425 Trp Lys Asp Ala Ser Gly Trp Ser Phe Ile Ala Gln Gln Lys Ser Asn 440 Leu Ile Thr Thr Met Glu Asn Thr Lys Phe Gly Gly Val Gly Thr Ser 455 450 Leu Ser Asp Ile Thr Ser Met Ala Glu Gly Glu Leu Ala Ala Lys Leu 470 Thr Ser Phe Met Phe Gly His Val Val Asn Phe Val Ile Ile Leu Ile Val Ile Leu Phe Leu Tyr Cys Met Ile Arg Asn Arg Asn Arg Gln Tyr 505 500 <210> 3 <211> 1464 <212> DNA <213> Baculovirus <220> <221> CDS <222> (1)..(1464) <400> 3 atq qta agc qct att gtt tta tat gtg ctt ttg gcg gcg gcg cat Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala His tct gcc ttt gcg gcg gag cac tgc aac gcg caa atg aag acg ggt ccg 96 Ser Ala Phe Ala Ala Glu His Cys Asn Ala Gln Met Lys Thr Gly Pro

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Lys Asp Val dlu Ile Thr Ile Val dlu Thr Asp Tyr Asn Glu Asn Val att atc ggc tac aag ggg tac tac cag gcg tat acg ggc aa acg ggc ggc Ile Ile Gly Tyr Lys Gly Tyr Tyr Gln Ala Tyr Ala Tyr Asn Gly Gly 65 70 75 80 tcg ctg gat ccc aac acc cgc gtc gaa gaa acc atg aaa acg ctg aat Ser Leu Asp Pro Asn Thr Arg Val Glu Glu Thr Met Lys Thr Leu Asn 85 90 gtg ggc aaa gag gat ttg ctt atg tgg agc atc agg cag cag tag gag Val Gly Lys Glu Asp Leu Leu Met Trp Ser Ile Arg Gln Gln Cys Glu 100 100 gtg ggc gaa gag ctg atc gac cgt tgg ggc agt gac agc gac gac tgt Val Gly Glu Clu Leu Ile Asp Arg Trp Gly Ser Asp Ser Asp Asp Cys 115 ttt cgc gac aac gag ggc cgc ggc cag tgg gtc aaa ggc aaa gag ttg Phe Arg Asp Asn Glu Gly Arg Gly Gln Trp Val Lys Gly Lys Glu Leu 130 135 gtg agc gaa at aac aat cac ttt gcg cac cac acg tgc aaa Val Lys Arg Gln Asn Asn Asn His Phe Ala His His Thr Cys Asn Lys 145 tcg tgg cga tgc ggc att tcc act tcg aaa atg tac agc agc tga Ser Trp Arg Cys Gly Ile Ser Thr Ser Lys Met Tyr Ser Arg Leu Glu 165 tcg tgg caa cac gaa gag agc gc gg gac agt gta tac att ttg gac gac gac Ser Trp Arg Cys Gly Ile Ser Thr Ser Lys Met Tyr Ser Arg Leu Glu 165 tgc cag gac gac acg acg gac tgc cag gta tac att ttg gac gac gac Ser Trp Arg Cys Gly Ile Ser Thr Ser Lys Met Tyr Ile Leu Asp Ala Glu 180 ggc aac ccc atc aac gtg acc Gtg gac cag gta tac att ttg gac gc tga gac Cys Gln Asp Asp Thr Asp Glu Cys Gln Val Tyr Ile Leu Asp Ala Glu 180 ggc aac ccc atc aac gtg acc gtg gac act gtg ctc cac gtg gac act Gly Asn Pro Ile Asn Val Thr Val Asp Thr Val Leu His Arg Asp Gly 195 205 gtg agt atg att cc aaa caa aag tct acg ttc acc acc cac acc gc caa ata Val Ser Met Ile Leu Lys Gln Lys Ser Thr Phe Thr Thr Arg Gln Ile 210 aaa gct gcg tgt ctg ctc att aaa gat gac aaa aat aac ccc gag tcg Lys Ala Ala Cys Leu Leu Ile Lys Asp Asp Lys Asn Asn Pro Glu Ser 225 gtg acc acc gaa cac ttt tt gat gac aat att att gat ctt tt Val Thr Arg Glu His Cys Leu Ile Asp Asn Asp Ile Tyr Asp Leu Ser			_	Ile				_	Ile		_		_	Glu	_	_		144
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Ser Leu Asp Pro Asn Thr Arg Val Glu Glu Thr Met Lys Thr Leu Asn 90 gtg ggc aaa gag gat ttg ctt atg tgg agc atc agg cag cag tgc gag 336 Val Gly Lys Glu Asp Leu Leu Met Trp Ser Ile Arg Gln Gln Cys Glu 100 gtg ggc gaa gag ctg atc gac cgt tgg ggc agt gac agc gac gac tgt 384 Val Gly Glu Glu Leu Ile Asp Arg Trp Gly Ser Asp Ser Asp Asp Cys 115 ttt cgc gac aac gag ggc cgc ggc cag tgg ggc aag ggc aaa gag ttg 432 Phe Arg Asp Asn Glu Gly Arg Gly Gln Trp Val Lys Gly Lys Glu Leu 130 gtg aag cgg cag aat aac aat cac ttt gcg cac cac acg tgc aac aaa Val Lys Arg Gln Asn Asn His Phe Ala His His Thr Cys Asn Lys 150 tcg tgg cga tgc ggc att tcc act tcg aaa atg tac agc agg ctc gag Ser Trp Arg Cys Gly Ile Ser Thr Ser Lys Met Tyr Ser Arg Leu Glu 165 tgc cag gac gac acg gac gag tgc cag tgg tat ac att ttg gac ac gc gag gct gag Ser Trp Arg Cys Gly Ile Ser Thr Ser Lys Met Tyr Ser Arg Leu Glu 170 ggc aac ccc atc aac gtg acc gtg gac act ttt gag tac att ttg gac gct gag 576 tgc cag gac gac acg gac gag tgc cag tgt gac act gtg cac act ttg aac act ttg gac gct gag 576 cys Gln Asp Asp Thr Asp Glu Cys Gln Val Tyr Ile Leu Asp Ala Glu 190 ggc aac ccc atc aac gtg acc gtg gac act gtg ctt cat cga gac gcc gdy Asn Pro Ile Asn Val Thr Val Asp Thr Val Leu His Arg Asp Gly 195 gtg agt atg att ctc aac caa aag tct acg ttc acc acg cgc caa ata 672 Val Ser Met Ile Leu Lys Gln Lys Ser Thr Phe Thr Thr Arg Gln Ile 210 aaa gct gcg tgt ctg ctc att aaa gat gac aaa aat aac ccc gag tcg 192 gtg aca cgc gac acc tgt ttg att gac aat gat ata tat gat ctt tct Ct Cval Thr Arg Glu His Cys Leu Ile Lys Asp Asp Ilys Asn Asn Pro Glu Ser 225 gtg aca cgc gac acc tgt ttg att gac aat gat ata tat gat ctt tct Cval Thr Arg Glu His Cys Leu Ile Asp Asn Asp Ile Tyr Asp Leu Ser		Ile					Gly					Tyr					Gly	240
The series of th						Asn					Glu					Leu		288
The first state of the first sta					Glu				_	Trp				_	Gln	_		336
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	·			-	Glu	His					Asn					Leu		768

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<212> PRT

<213> Baculovirus

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35 40 45

Lys Asp Val Glu Ile Thr Ile Val Glu Thr Asp Tyr Asn Glu Asn Val 50 55 60

Ile Ile Gly Tyr Lys Gly Tyr Tyr Gln Ala Tyr Ala Tyr Asn Gly Gly 65 70 75 80

Ser Leu Asp Pro Asn Thr Arg Val Glu Glu Thr Met Lys Thr Leu Asn 85 90 95

Val Gly Lys Glu Asp Leu Leu Met Trp Ser Ile Arg Gln Gln Cys Glu 100 105 110

Val Gly Glu Glu Leu Ile Asp Arg Trp Gly Ser Asp Ser Asp Cys 115 120 125

Phe Arg Asp Asn Glu Gly Arg Gly Gln Trp Val Lys Gly Lys Glu Leu 130 135 140

Val Lys Arg Gln Asn Asn Asn His Phe Ala His His Thr Cys Asn Lys 145 150 155 160

Ser Trp Arg Cys Gly Ile Ser Thr Ser Lys Met Tyr Ser Arg Leu Glu 165 170 175

Cys Gln Asp Asp Thr Asp Glu Cys Gln Val Tyr Ile Leu Asp Ala Glu 180 185 190

Gly Asn Pro Ile Asn Val Thr Val Asp Thr Val Leu His Arg Asp Gly
195 200 205

Val Ser Met Ile Leu Lys Gln Lys Ser Thr Phe Thr Thr Arg Gln Ile 210 215 220

Lys Ala Ala Cys Leu Leu Ile Lys Asp Asp Lys Asn Asn Pro Glu Ser 225 230 235 240

Val Thr Arg Glu His Cys Leu Ile Asp Asn Asp Ile Tyr Asp Leu Ser 245 250 255 Lys Asn Thr Trp Asn Cys Lys Phe Asn Arg Cys Ile Lys Arg Lys Val 260 265 270

Glu His Arg Val Lys Lys Arg Pro Pro Thr Trp Arg His Asn Val Arg 275 280 285

Ala Lys Tyr Thr Glu Gly Asp Thr Ala Thr Lys Gly Asp Leu Met His 290 295 300

Ile Gln Glu Glu Leu Met Tyr Glu Asn Asp Leu Leu Lys Met Asn Ile 305 310 315

Glu Leu Met His Ala His Ile Asn Lys Leu Asn Asn Met Leu His Asp 325 330 335

Leu Ile Val Ser Val Ala Lys Val Asp Glu Arg Leu Ile Gly Asn Leu 340 345 350

Met Asn Asn Ser Val Ser Ser Thr Phe Leu Ser Asp Asp Thr Phe Leu 355 360 365

Leu Met Pro Cys Thr Asn Pro Pro Ala His Thr Ser Asn Cys Tyr Asn 370 375 380

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Gln Cys Ile Asp Phe Ser Asn Tyr Lys Glu Leu Ala Ile Asp Asp Asp 405 410 415

Val Glu Phe Trp Ile Pro Thr Ile Gly Asn Thr Thr Tyr His Asp Ser 420 425 430

Trp Lys Asp Ala Ser Gly Trp Ser Phe Ile Ala Gln Gln Lys Ser Asn 435 440 445

Leu Ile Thr Thr Met Glu Asn Thr Lys Phe Gly Gly Val Gly Thr Ser 450 455 460

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Thr Ser Phe Met Phe Gly His Val 485

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                                                                     97
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Ala Ala His Ser Ala Phe Ala Ala Glu His Cys Asn Ala Gln Met Lys
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gaa Glu 65	aac Asn	gtg Val	att Ile	atc Ile	ggc Gly 70	tac Tyr	aag Lys	ggg Gly	tac Tyr	tac Tyr 75	cag Gln	gcg Ala	tat Tyr	gcg Ala	tac Tyr 80	241
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acg Thr	ctg Leu	aat Asn	gtg Val 100	ggc Gly	aaa Lys	gag Glu	gat Asp	ttg Leu 105	ctt Leu	atg Met	tgg Trp	agc Ser	atc Ile 110	agg Arg	cag Gln	337
					gaa Glu											385
gac Asp	gac Asp 130	tgt Cys	ttt Phe	cgc Arg	gac Asp	aac Asn 135	gag Glu	ggc Gly	cgc Arg	ggc Gly	cag Gln 140	tgg Trp	gtc Val	aaa Lys	ggc	433
aaa Lys 145	gag Glu	ttg Leu	gtg Val	aag Lys	cgg Arg 150	cag Gln	aat Asn	aac Asn	aat Asn	cac His 155	ttt Phe	gcg Ala	cac His	cac His	acg Thr 160	481
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	aaa Lys															865
	gtt Val 290															913
	atg Met															961
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	acc Thr															1441
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Thr Leu Gln Lys Asp Val Glu Ile Thr Ile Val Glu Thr Asp Tyr Asn 50 60

Glu Asn Val Ile Ile Gly Tyr Lys Gly Tyr Tyr Gln Ala Tyr Ala Tyr 65 70 75 80

Asn Gly Gly Ser Leu Asp Pro Asn Thr Arg Val Glu Glu Thr Met Lys 85 90 95

Thr Leu Asn Val Gly Lys Glu Asp Leu Leu Met Trp Ser Ile Arg Gln
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Gln Cys Glu Val Gly Glu Glu Leu Ile Asp Arg Trp Gly Ser Asp Ser 115 120 125

Asp Asp Cys Phe Arg Asp Asn Glu Gly Arg Gly Gln Trp Val Lys Gly 130 135 140

Lys Glu Leu Val Lys Arg Gln Asn Asn Asn His Phe Ala His His Thr 145 150 155 160

Cys Asn Lys Ser Trp Arg Cys Gly Ile Ser Thr Ser Lys Met Tyr Ser 165 170 175

Arg Leu Glu Cys Gln Asp Asp Thr Asp Glu Cys Gln Val Tyr Ile Leu 180 185 190 Asp Ala Glu Gly Asn Pro Ile Asn Val Thr Val Asp Thr Val Leu His
195 200 205

Arg Asp Gly Val Ser Met Ile Leu Lys Gln Lys Ser Thr Phe Thr Thr 210 215 220

Arg Gln Ile Lys Ala Ala Cys Leu Leu Ile Lys Asp Asp Lys Asn Asn 225 230 235 240

Pro Glu Ser Val Thr Arg Glu His Cys Leu Ile Asp Asn Asp Ile Tyr 245 250 255

Asp Leu Ser Lys Asn Thr Trp Asn Cys Lys Phe Asn Arg Cys Ile Lys 260 265 270

Arg Lys Val Glu His Arg Val Lys Lys Arg Pro Pro Thr Trp Arg His 275 280 285

Asn Val Arg Ala Lys Tyr Thr Glu Gly Asp Thr Ala Thr Lys Gly Asp 290 295 300

Leu Met His Ile Gln Glu Glu Leu Met Tyr Glu Asn Asp Leu Leu Lys 305 310 315

Met Asn Ile Glu Leu Met His Ala His Ile Asn Lys Leu Asn Asn Met 325 330 335

Leu His Asp Leu Ile Val Ser Val Ala Lys Val Asp Glu Arg Leu Ile 340 345 350

Gly Asn Leu Met Asn Asn Ser Val Ser Ser Thr Phe Leu Ser Asp Asp 355 360 365

Thr Phe Leu Leu Met Pro Cys Thr Asn Pro Pro Ala His Thr Ser Asn 370 375 380

Cys Tyr Asn Asn Ser Ile Tyr Lys Glu Gly Arg Trp Val Ala Asn Thr 385 390 395 400

Asp Ser Ser Gln Cys Ile Asp Phe Ser Asn Tyr Lys Glu Leu Ala Ile 405 410 415 Asp Asp Asp Val Glu Phe Trp Ile Pro Thr Ile Gly Asn Thr Thr Tyr 420 425 430

His Asp Ser Trp Lys Asp Ala Ser Gly Trp Ser Phe Ile Ala Gln Gln 435 440 445

Lys Ser Asn Leu Ile Thr Thr Met Glu Asn Thr Lys Phe Gly Gly Val 450 455 460

Gly Thr Ser Leu Ser Asp Ile Thr Ser Met Ala Glu Gly Glu Leu Ala 465 470 475 480

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